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Conference Abstract

Design and use of NOMEN, an ontology defining the rules of biological nomenclature

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Abstract

The most complex nomenclatural databases are developed not from community based efforts but from individuals who have encoded their understanding of the rules of nomenclature into bespoke knowledge-bases. In efforts spanning decades well over 75 types of “status” may to be defined for a single database. Reconciliation of these status types into new, federated systems is nearly always the most difficult aspect of their migration. Nomenclatural data is often recorded in a logically inconsistent manner, for example mixing governed rules and curator annotations. NOMEN (https://github.com/SpeciesFileGroup/nomen) is an Web Ontology Language (OWL) ontology that seeks to address these issues, providing standardized URIs for classes of nomenclatural annotations on taxonomic names (not taxonomic concepts). It includes assertions for the animal (ICZN), plant (ICN), and bacterial (ICNB) codes. NOMEN based assertions can be encoded in a simple graph format, as illustrated in its implementation in TaxonWorks (http://taxonworks.org). We illustrate its application within the migration process of four very large taxonomic databases.

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Keywords

ontology, biological nomenclature, OWL, application, ICZN, ICN

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